

Package ‘FGRepo’

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Type Package

Title Functional Genomics Repository for POST-GWAS Analysis

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Depends R (>= 3.5)

Description A collection of datasets essential for functional genomic analysis. Gene names, gene positions, cytoband information, sourced from Ensembl and phenotypes association graph prepared from GWAScatalog are included. Data is available in both GRCh37 and 38 builds. These datasets facilitate a wide range of genomic studies, including the identification of genetic variants, exploration of genomic features, and post-GWAS functional analysis.

License GPL-3

Encoding UTF-8

LazyData true

LazyDataCompression xz

RoxygenNote 7.3.2

NeedsCompilation no

Repository CRAN

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cytoband_grch37	<i>Cytoband information (GRCh37)</i>
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Description

A dataset containing cytoband information based on GRCh37.

Usage

cytoband_grch37

Format

A data frame with 4 columns:

- chr** chromosome
- start** start position
- end** end position
- band** band name

Source

Ensembl, <https://www.ensembl.org>

References

Harrison, PW, et al. (2024). Ensembl 2024. Nucleic Acids Research, 52, Pages D891–D899.
[doi:10.1093/nar/gkad1049](https://doi.org/10.1093/nar/gkad1049)

Examples

data(cytoband_grch37)

cytoband_grch38	<i>Cytoband information (GRCh38)</i>
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Description

A dataset containing cytoband information based on GRCh38.

Usage

cytoband_grch38

Format

A data frame with 4 columns:

- chr** chromosome
- start** start position
- end** end position
- band** band name

Source

Ensembl, <https://www.ensembl.org>

References

Harrison, PW, et al. (2024). Ensembl 2024. Nucleic Acids Research, 52, Pages D891–D899. [doi:10.1093/nar/gkad1049](https://doi.org/10.1093/nar/gkad1049)

Examples

```
data(cytoband_grch38)
```

gene_names_grch37	<i>Gene Names (GRCh37)</i>
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Description

A dataset containing gene names based on GRCh37.

Usage

```
gene_names_grch37
```

Format

A data frame with 6 columns:

- id** Gene identifier
- name** Gene name
- chr** Chromosome
- start** Start position
- end** End position
- type** Gene type

Source

Ensembl, <https://www.ensembl.org>

References

Harrison, PW, et al. (2024). Ensembl 2024. Nucleic Acids Research, 52, Pages D891–D899.
[doi:10.1093/nar/gkad1049](https://doi.org/10.1093/nar/gkad1049)

Examples

```
data(gene_names_grch37)
```

gene_names_grch38	<i>Gene Names (GRCh38)</i>
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Description

A dataset containing gene names based on GRCh38.

Usage

```
gene_names_grch38
```

Format

A data frame with 6 columns:

id Gene identifier

name Gene name

chr Gene name

start Gene name

end Gene name

type Gene name

Source

Ensembl, <https://www.ensembl.org>

References

Harrison, PW, et al. (2024). Ensembl 2024. Nucleic Acids Research, 52, Pages D891–D899.
[doi:10.1093/nar/gkad1049](https://doi.org/10.1093/nar/gkad1049)

Examples

```
data(gene_names_grch38)
```

GWASCat_graph*GWAScatalog graph*

Description

A graph object of GWAScatalog data. The association between variants and phenotypes are indicated.

Usage

```
GWASCat_graph
```

Format

An object of igraph class.

Source

GWAS Catalog, <https://www.ebi.ac.uk/gwas>

References

Sollis, E, et al. (2022). The NHGRI-EBI GWAS Catalog: knowledgebase and deposition resource. Nucleic Acids Research, 51, Pages D977–D985. [doi:10.1093/nar/gkac1010](https://doi.org/10.1093/nar/gkac1010)

Examples

```
data(GWASCat_graph)
```

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